

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 11, 2004, 14:20:50 ; Search time 18 Seconds
(without alignments)
1307.539 Million cell updates/sec

Title: US-09-787-678A-1
Perfect score: 2314
Sequence: 1 MAAALRSWCRCPRCLGS.....NPYAAWRLLDISASSTEQIL 452

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2314	100.0	452	1	IM44 HUMAN
2	212.5	91.3	453	1	IM44 RAT
3	2108	91.1	452	1	IM44 MOUSE
4	918.5	39.7	425	1	IM44 CAEL
5	441.5	19.1	427	1	IM44 SCHPO
6	406	17.5	431	1	IM44 YEAST
7	141	6.1	1093	1	TMF1 HUMAN
8	140.5	6.1	612	1	RPSD BUCAL
9	140.5	6.1	879	1	RA50 PYRHO
10	139	6.0	978	1	RA50 AQUAE
11	137.5	5.9	3259	1	GOB1 HUMAN
12	134.5	5.8	658	1	VAT1 METH
13	133.5	5.8	2116	1	MY52 DICDI
14	133	5.7	2663	1	CENE HUMAN
15	132.5	5.7	808	1	Y066 NPVAC
16	132.5	5.7	1939	1	MYH1 HUMAN
17	132	5.7	478	1	GAS8 HUMAN
18	132	5.7	1940	1	MYH3 RAT
19	131.5	5.7	1203	1	SMC2 XENLA
20	131.5	5.7	8797	1	SNE1 HUMAN
21	130.5	5.6	919	1	RA50 AERPE
22	130.5	5.6	1169	1	SMC METVA
23	130	5.6	852	1	RA50 THEMA
24	130	5.6	2017	1	MY5N DROME
25	129.5	5.6	1433	1	REST CHICK
26	129.5	5.6	1957	1	SPOF SCHPO
27	129	5.6	1938	1	MYHD HUMAN
28	128.5	5.6	1114	1	RH18 YEAST
29	128	5.5	851	1	YD72 SCHPO
30	127.5	5.5	520	1	REC N AQUAE
31	127.5	5.5	1288	1	SMC4 HUMAN
32	127	5.5	1182	1	CGA2 HELPY
33	127	5.5	1940	1	MYH3 HUMAN

34	127	5.5	2867	1	RBP2 PLAYB
35	126.5	5.5	1940	1	MYH3-CHICK
36	126	5.4	1163	1	SBCC-CLOAB
37	125.5	5.4	1790	1	USO1 YEAST
38	125	5.4	811	1	HSP7 YEAST
39	125	5.4	2230	1	GOA4 HUMAN
40	125	5.4	4687	1	PLE1 RAT
41	124.5	5.4	1938	1	MYSS-CHICK
42	124.5	5.4	1939	1	MYH4 HUMAN
43	124	5.4	541	1	EH44 MOUSE
44	124	5.4	875	1	ZIP1 YEAST
45	124	5.4	1046	1	SBCC-LACLA

ALIGNMENTS

RESULT 1
IM44 HUMAN
ID IM44 HUMAN STANDARD; PRT; 452 AA.
AC O43615; ORN193;
DT 15-JUL-1999 (Rel. 38, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Import inner membrane translocase subunit TIM44, mitochondrial precursor.
DE TIM44 OR MIMT44 OR TIM44.
GN Homo sapiens (Human)
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
[1]
RP SEQUENCE FROM N.A.
RC TISSUE=Skeletal muscle;
RX MEDLINE=99272555; PubMed=10339406;
RA Bauer M.F., Gempel K., Reichert A.S., Rappold G.A., Lichtner P., Gerbitz K.D., Neupert W., Brunner M., Hofmann S.
RT "Genetic and structural characterization of the human mitochondrial inner membrane translocase".
RL J. Mol. Biol. 289:69-82(1999). MAY
[2]
SEQUENCE FROM N.A.
RP TISSUE=Brain;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Brownstein M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Raha S.S., Loquellano N.A., Peters G.J., Carninci P., Prange C., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huiyk S.W., Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A., Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butler A., Schein J.E., Jones S.J.M., Skalska U., Smalish D.E., Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences".
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -!- FUNCTION: Involved in protein import into the mitochondrion. Probably involved in translocation across the inner membrane. As a binding protein required for driving the import of preproteins. Recruits mitochondrial HSP70 to drive protein translocation into the matrix using ATP as an energy source.
CC -!- SUBUNIT: Forms part of the receptor complex that consists of at least 3 different proteins (TIM17, TIM23, TIM44) (By similarity).
CC -!- SUBCELLULAR LOCATION: Mitochondrial inner membrane.
CC -!- SIMILARITY: Belongs to the Tim44 family.

Q00799	plasmodium
P02565	gallus gall
Q97fki	clostridium
P23386	saccharomyc
P33416	saccharomyc
Q13439	homo sapien
P30427	rattus norv
P13538	gallus gall
Q9Y623	homo sapien
Q9eqp2	mus musculu
P31111	saccharomyc
Q9cfz0	lactococcus

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 CC -----
 DE EMBL; AF041254; AAH97740.1; --
 DE EMBL; BC033628; AAH33628.1; --
 DE Genew; HGNC:17316; TIMM44.
 DE MIM; 605058; --
 DE GO; GO:0005759; C-mitochondrial matrix; TAS.
 DE GO; GO:0006628; P-mitochondrial translocation; TAS.
 DE InterPro; IPR007379; Tim44.
 DE InterPro; IPR005682; Tim44_sub.
 DE Pfam; PF04280; Tim44; 1.
 DE TIGRFAMs; TIGR00984; 3a0801s03tim44; 1.
 DE Mitochondrion; Inner membrane; Transport; Protein transport;
 DE Translocation; Transmembrane; Transmembrane; ATP-binding;
 DE TRANSIT ?
 DE CHAIN ? 453
 DE IMPORT INNER MEMBRANE TRANSLOCASE SUBUNIT
 DE TIM44.
 DE NP_BIND 166 173
 DE CONFLICT 189 189
 DE CONFLICT 226 226
 DE SEQUENCE 452 AA; 51355 MW; 15BECF875611BE96 CRC64;

Query Match 100.0%; Score 2314; DB 1; Length 452;
 Best Local Similarity 100.0%; Pred. No. 1.1e-117;
 Matches 452; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAAALRGWCRCPRCLGSGIQFLSSHNLPQSTYQMRPGLPGLSKSYSSGNRKGFL 60
 DB 1 MAAALRGWCRCPRCLGSGIQFLSSHNLPQSTYQMRPGLPGLSKSYSSGNRKGFL 60
 QY 61 SGLLDNVKQELAKNKKEMKESIKKFRDEARRLEESDVLQEARRYKKTIESVTRSEVLRK 120
 DB 61 SGLLDNVKQELAKNKKEMKESIKKFRDEARRLEESDVLQEARRYKKTIESVTRSEVLRK 120
 QY 121 KLGLTGTVKESLHEVSKSDLRKIKGVVEAAKTAQSAESVSKGEGKLGRFAAFRLS 180
 DB 121 KLGLTGTVKESLHEVSKSDLRKIKGVVEAAKTAQSAESVSKGEGKLGRFAAFRLS 180
 QY 181 QGVESVKKIDSDVLGQGTGPRPQRLKRTFAGDKFKEKVFEPNEEALGVVLHKDSK 240
 DB 181 QGVESVKKIDSDVLGQGTGPRPQRLKRTFAGDKFKEKVFEPNEEALGVVLHKDSK 240
 QY 241 WYQWKDFKNNVFNFRFFEMKMKYDESDNAFTRASRALTDKVTDLGLFSKTEMSEVL 300
 DB 241 WYQWKDFKNNVFNFRFFEMKMKYDESDNAFTRASRALTDKVTDLGLFSKTEMSEVL 300
 QY 301 TEILRVDPAPDKDRFLKQCENDIIPNVLEAMISGELDIKDWCEATYSQLAHPITQOAKA 360
 DB 301 TEILRVDPAPDKDRFLKQCENDIIPNVLEAMISGELDIKDWCEATYSQLAHPITQOAKA 360
 QY 361 LGLQPHSRILDDNVDLAMGKWEQGPVLIITFOALVWVRNPKGEVVEGDPDKVLRML 420
 DB 361 LGLQPHSRILDDNVDLAMGKWEQGPVLIITFOALVWVRNPKGEVVEGDPDKVLRML 420
 QY 421 YWALCRQDDELNPYAAWRLDIDISASSTEQIL 452
 DB 421 YWALCRQDDELNPYAAWRLDIDISASSTEQIL 452

RESULT 2
 ID IM44_RAT
 AC O35094
 DT 15-JUL-1999 (Rel. 38, Created)
 DT 15-JUL-1999 (Rel. 38, Last sequence update)
 DT 15-MAR-2004 (Rel. 43, Last annotation update)

DE Import inner membrane translocase subunit TIM44, mitochondrial
 DE precursor.
 DE GN TIMM44 OR TIMM44 OR TIM44.
 DE OS Rattus norvegicus (Rat).
 DE OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 DE OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 DE OX NCBI_TaxID=10116;
 DE RN [1]
 DE RP SEQUENCE FROM N.A.
 DE RC TISSUE=Liver;
 DE RX MEDLINE=98207064; PubMed=9538267;
 DE RA Ishihara N., Mihara K.;
 DE RT "Identification of the protein import components of the rat
 DE RT mitochondrial inner membrane, rTIM17, rTIM23, and rTIM44.";
 DE RL J. Biochem. 123:722-732(1998).
 DE CC -!- FUNCTION: Involved in protein import into the mitochondrion.
 DE CC Probably involved in translocation across the inner membrane. As a
 DE CC binding protein required for driving the import of preproteins.
 DE CC Recruits mitochondrial HSP70 to drive protein translocation into
 DE CC the matrix using ATP as an energy source.
 DE CC -!- SUBUNIT: Forms part of the receptor complex that consists of at
 DE CC least 3 different proteins (TIM17, TIM23, TIM44) (By similarity).
 DE CC -!- SUBCELLULAR LOCATION: Mitochondrial inner membrane.
 DE CC -!- SIMILARITY: Belongs to the Tim44 family.
 DE CC -----
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 DE CC -----
 DE EMBL; AB006452; BAA21820.1; --
 DE PTR; JE0155; JE0155.
 DE InterPro; IPR007379; Tim44.
 DE InterPro; IPR005682; Tim44_sub.
 DE Pfam; PF04280; Tim44; 1.
 DE TIGRFAMs; TIGR00984; 3a0801s03tim44; 1.
 DE Mitochondrion; Inner membrane; Transport; Protein transport;
 DE Translocation; Transmembrane; Transmembrane; ATP-binding;
 DE TRANSIT ? 453
 DE CHAIN ? 453
 DE IMPORT INNER MEMBRANE TRANSLOCASE SUBUNIT
 DE TIM44.
 DE NP_BIND 167 174
 DE SEQUENCE 453 AA; 51060 MW; 387C685147C577A0 CRC64;
 SQ
 Query Match 91.3%; Score 2112.5; DB 1; Length 453;
 Best Local Similarity 90.1%; Pred. No. 7.7e-107;
 Matches 408; Conservative 24; Mismatches 20; Indels 1; Gaps 1;
 QY 1 MAAALRGWCRCPRCLGSGIQFLSSHNLPQSTYQMRPGLPGLSKSYSSGNRKGFL 59
 DB 1 MAAALRGWCRCPRCLGSGIQFLSSHNLPQSTYQMRPGLPGLSKSYSSGNRKGFL 60
 QY 60 SGLLDNVKQELAKNKKEMKESIKKFRDEARRLEESDVLQEARRYKKTIESVTRSEVLR 119
 DB 61 SGLLDNVKQELAKNKKEMKESIKKFRDEARRLEESDVLQEARRYKKTIESVTRSEVLR 120
 QY 120 KLGLTGTVKESLHEVSKSDLRKIKGVVEAAKTAQSAESVSKGEGKLGRFAAFRLS 179
 DB 121 KLGLTGTVKESLHEVSKSDLRKIKGVVEAAKTAQSAESVSKGEGKLGRFAAFRLS 180
 QY 180 SQGVESVKKIDSDVLGQGTGPRPQRLKRTFAGDKFKEKVFEPNEEALGVVLHKDS 239
 DB 181 SQGVESVKKIDSDVLGQGTGPRPQRLKRTFAGDKFKEKVFEPNEEALGVVLHKDS 240
 QY 240 KWKQWKDFKNNVFNFRFFEMKMKYDESDNAFTRASRALTDKVTDLGLFSKTEMSEV 299
 DB 241 KWKQWKDFKNNVFNFRFFEMKMKYDESDNAFTRASRALTDKVTDLGLFSKTEMSEV 300
 QY 300 LTELVRDPAPDKDRFLKQCENDIIPNVLEAMISGELDIKDWCEATYSQLAHPITQOAK 359